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McLoughlin, N.M.; Mueller, C.; Grossmann, T.N.

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# The Therapeutic Potential of PTEN Modulation: Targeting Strategies from Gene to Protein

Niall M. McLoughlin,<sup>1</sup> Carolin Mueller,<sup>1</sup> and Tom N. Grossmann<sup>1,2,\*</sup>

<sup>1</sup>Department of Chemistry and Pharmaceutical Sciences, VU University Amsterdam, 1081 HZ Amsterdam, the Netherlands

<sup>2</sup>Chemical Genomics Centre of the Max Planck Society, 44227 Dortmund, Germany

\*Correspondence: [t.n.grossmann@vu.nl](mailto:t.n.grossmann@vu.nl)

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Two decades have passed since the discovery of the tumor suppressor, PTEN. A multitude of biological functions have since been revealed, suggesting potential therapeutic applications for both PTEN activation (e.g., cancer) and inhibition (e.g., neuroregeneration). Nevertheless, PTEN's therapeutic suitability has been called into question due to its “risky” profile as a tumor suppressor. To evaluate PTEN function and its various roles in disease a number of molecules have so far been developed. However, intrinsic problems associated with phosphatase inhibition and PTEN's complex regulation via post-translational modifications hinder straightforward access to selective modulators. For this reason, central questions associated with PTEN targeting remain unanswered. In this perspective, we summarize current PTEN-targeting strategies and discuss potential approaches to modulate its functional dose, considering all stages of PTEN biogenesis from direct protein modulation to the targeting of relevant miRNAs as well as the *PTEN* gene and mRNA.

## Introduction

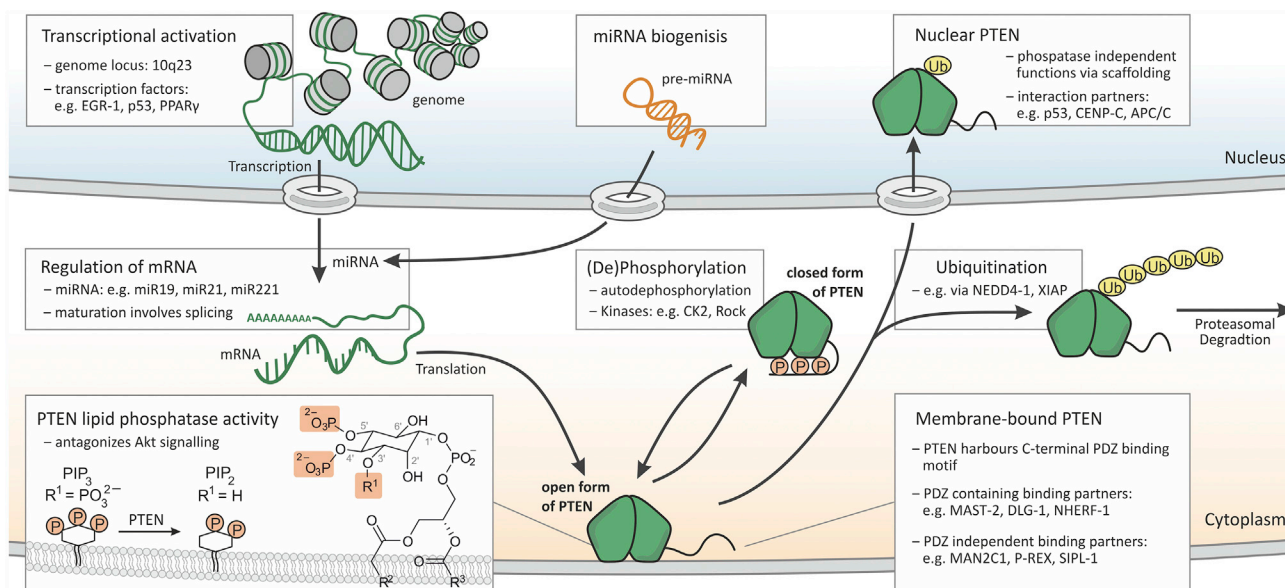
In 1997, a phosphatase-encoding gene, which upon deletion induced aggressive tumorigenesis across kidney, breast and prostate cell lines (Li et al., 1997; Steck et al., 1997), was identified. Phosphatase and Tensin Homolog on Chromosome 10 (PTEN) was quickly validated as an essential tumor suppressor and over the course of the next two decades, characterized as a ubiquitous modulator of cell growth and proliferation, features mainly associated with its lipid phosphatase activity (Salmena, 2016). After *p53*, *PTEN* is the second most commonly mutated tumor suppressor in human cancer with some 30% of tumors harboring somatic, *PTEN* mutations (Nakamura et al., 2000; Simpson and Parsons, 2001). In addition, *PTEN* dysregulation has been implicated not only in cancer but in a wide variety of other non-oncogenic illnesses, including Alzheimer's disease and autism (Knafo et al., 2016; Zhou and Parada, 2012).

*PTEN* at the 10q23 locus is under the control of various transcription factors such as EGR-1, p53, ATF2, PPAR $\gamma$  (Correia et al., 2014). Other proteins such as HES-1, C-Jun, and NF- $\kappa$ B transcriptionally repress *PTEN*, while an additional layer of epigenetic repression has also been reported to occur via methylation of the *PTEN* promoter or via histone deacetylase-containing complexes such as PML/RAR $\alpha$  or NuRD/Mi2 (Correia et al., 2014; Lu et al., 2009; Noguera et al., 2016). Upon transcription, *PTEN* mRNA undergoes splicing and is translocated to the cytosol where it becomes a target for miRNA-guided degradation (Sharrard and Maitland, 2000) (Figure 1). Prominent *PTEN*-targeting miRNAs include proto-oncogenic miR-19, miR-21, and miR-221 (Garofalo et al., 2009; Meng et al., 2007; Olive et al., 2009). As an added layer of regulatory complexity, several long non-coding RNAs (lncRNAs) purportedly sequester miRNAs from binding to *PTEN* mRNA, however the biological significance of this mechanism remains contro-

versial (Poliseno et al., 2010; Tay et al., 2011; Thomson and Dinger, 2016).

PTEN is a protein containing 403 amino acids with a number of additional proteoforms (Malaney et al., 2017). It fulfills its main tumor suppressor activity at the plasma membrane by dephosphorylating phosphatidylinositol (3,4,5)-trisphosphate (PIP<sub>3</sub>, Figure 1) to phosphatidylinositol-4,5-bisphosphate (PIP<sub>2</sub>) (Song et al., 2012) thereby counteracting phosphoinositide 3-kinase (PI3K) signaling (Jean and Kiger, 2014). Among others (Rowland et al., 2011), PTEN inhibits AKT-dependent pathways such as GSK3 (metabolic stimulation), FOXO (cell cycle progression), BAD/MDM2 (cell survival), and the mTOR axis (protein synthesis) (Song et al., 2012). Critically, PTEN's phosphatase activity and subcellular localization are dynamically controlled by post-translational modifications (PTMs) (Bermúdez Brito et al., 2015), examples include phosphorylation, ubiquitination, oxidation, acetylation, and sumoylation (Bermúdez Brito et al., 2015). Phosphorylation of PTEN's C-tail promotes electrostatic interactions with its membrane-binding region, resulting in a conformationally closed state with reduced membrane association and phosphatase activity (Silva et al., 2008) (Figure 1). While not fully elucidated, autodephosphorylation contributes to the conformational re-opening of PTEN (Rahdar et al., 2009; Tibarewal et al., 2012). Monoubiquitination by NEDD4-1 promotes nuclear import, whereas polyubiquitination by the same enzyme or others marks PTEN for proteasomal degradation (Leslie et al., 2016). Certain PTMs can also mediate direct inhibition of phosphatase activity as seen when PTEN's catalytic cysteine is oxidized by reactive oxygen species (Cho et al., 2004; Lee et al., 2015).

Aside from PIP<sub>3</sub> dephosphorylation and autodephosphorylation, PTEN recognizes other protein substrates and is involved in a number of protein-protein interactions (PPIs) (Myers et al., 1997; Worby and Dixon, 2014). PPIs involving



**Figure 1. Schematic Overview of PTEN Biogenesis and Regulation**

Located at chromosome 10q23, *PTEN* is transcribed under the influence of various transcription factors, including EGR-1, p53 and PPAR $\gamma$ . Upon transcription, *PTEN* mRNA is spliced and becomes a target for a number of miRNAs, including miR-21. Translation yields the PTEN protein, a membrane-active lipid phosphatase that primarily dephosphorylates PIP $_3$  to provide PIP $_2$  thereby antagonizing AKT signaling. Membrane-localized PTEN also engages in a number of protein-protein interactions (PPIs) with PDZ-containing proteins through its C-tail domain. PTMs modulate both PTEN's enzymatic activity and cellular localization. Via phosphorylation of its C-tail, PTEN enters a conformationally closed state, which promotes membrane dissociation. In contrast, mono-ubiquitination can promote nuclear localization where PTEN may act via phosphatase-dependent or -independent mechanisms. Poly-ubiquitination promotes PTEN degradation.

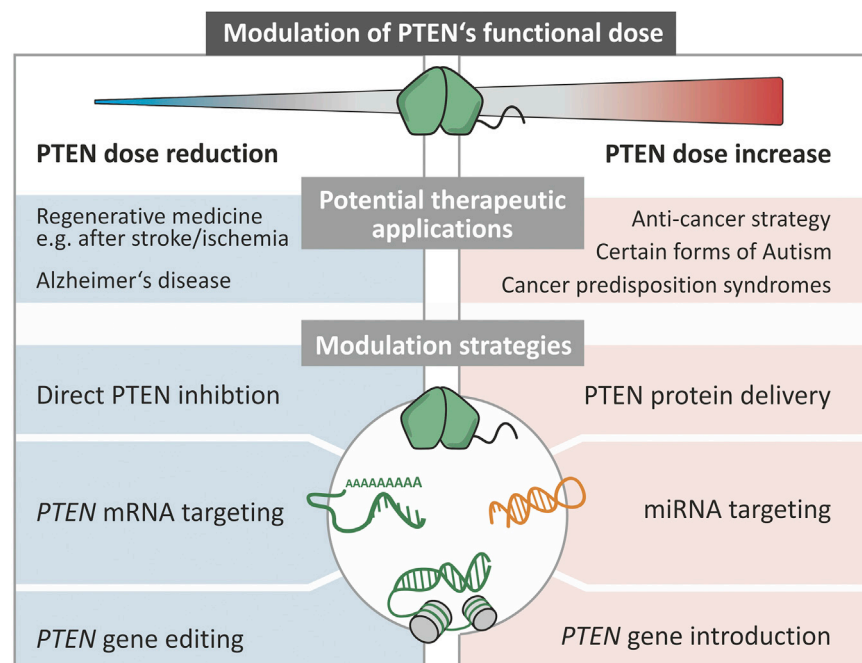
PTEN's PDZ-binding motif at the plasma membrane often enhance PTEN's phosphatase activity (e.g., interactions with DLG1, MAST2, or NHERF1) while PPIs involving PTEN's C2 or phosphatase domains are known to repress enzymatic activity (e.g., PREX2a, SIPL1, or Man2C1 interactions) (Worby and Dixon, 2014). In the nucleus, PTEN-mediated PPIs enhance the activity of numerous protein substrates such as the kinetochore-binding protein CENP-C, the E3 ubiquitin ligase APC/C as well as p53 (Worby and Dixon, 2014). In general, these nuclear interactions have been shown to benefit chromosomal stability and healthy cell-cycle progression (Worby and Dixon, 2014). However, it remains unclear whether PTEN's phosphatase activity acts in concert with these effects.

The modulation of PTEN activity and/or protein levels is considered a potential therapeutic strategy for a number of disease states. To describe the overall amount of PTEN capable of engaging in both phosphatase-dependent and -independent activities, the term “functional dose” has been introduced (Berger et al., 2011). Given PTEN's central role in the regulation of cell growth and proliferation, changes to its functional dose trigger profound biological effects that are expected to be of therapeutic use (Figure 2) (Alimonti et al., 2010). A reduction of PTEN's functional dose can promote cell growth and proliferation and is considered beneficial in regenerative medicine, e.g., after stroke or ischemia, and in Alzheimer's disease. However, it is not clear to what extent such strategies may induce cancer formation. On the other hand, increasing PTEN's functional dose and thereby promoting its tumor suppressor activity has been pursued for the development of anti-cancer therapies, the treatment of certain forms of autism as well as cancer predisposition syndromes.

In this perspective, we summarize available strategies for both reduction and increase of functional dose, considering all stages of PTEN biogenesis from direct protein modulation to the targeting of relevant miRNAs as well as the *PTEN* gene and mRNA (Figure 2, bottom). In addition, emerging technologies are highlighted that could provide valuable, PTEN-targeting strategies. We conclude with a general discussion of PTEN's potential as a therapeutic target and the risks associated with its central tumor suppressor function.

### Reduction of PTEN's Functional Dose

The reduction of PTEN's functional dose has garnered interest in the context of tissue regeneration, given PTEN's central role as an antagonist of AKT-mediated cell growth and proliferation. In the nervous system where tissue (re)growth is intrinsically protracted, conditional PTEN deletion (and subsequent mTOR activation) has been shown to promote axon regeneration after crush injuries in both optical and spinal neurons (Liu et al., 2010; Park et al., 2008; Sun et al., 2011). Analogously, conditional PTEN deletion benefits cardiomyocyte survival by preventing ischemia and limiting reperfusion (Bird et al., 2014; Ruan et al., 2009). Collectively, these findings have shaped PTEN's profile as a therapeutic target after stroke and nerve injuries. PTEN dose reduction may also find application in the context of Alzheimer's disease. As recently shown, PTEN silencing or inhibition of PTEN membrane localization at synapses affected by  $\beta$ -amyloid aggregation leads to strong reductions in Alzheimer-mediated cognitive deficiencies (Knafo et al., 2016). Approaches to reduce PTEN's functional dose involve direct protein inhibition, the targeting of *PTEN* mRNA, and anti-gene strategies (Figure 2).



**Figure 2. Overview of Potential Therapeutic Applications and Strategies Toward PTEN Modulation**

enzymes (Costa Pessoa et al., 2015). Vanadyl (VO) complexes such as VO-OHpic (Figure 3C), have also been shown to inhibit PTEN phosphatase activity *in vitro* (half maximal inhibitory concentration, 35 nM) while triggering increased PIP<sub>3</sub> levels and AKT translocation in NIH 3T3 fibroblasts (Rosivatz et al., 2006). Unlike bpVs, VO complexes are suggested to inhibit phosphatases through a reversible, non-oxidative mechanism, a feature recently exploited for activity-based, phosphatase imaging probes (Collins et al., 2016). Aside from vanadium-based complexes, SF1670 and the naphthoquinone-derived natural product Shikonin have been reported to inhibit PTEN's phosphatase activity (Figure 3E), likely through irreversible

### Direct Targeting of PTEN Function

PTEN is translated as a 403 residue protein comprised of a central phosphatase and C2 domain flanked by flexible regulatory tails (Figure 3A) (Lee et al., 1999). The phosphatase domain harbors a highly conserved active site around the catalytic cysteine (C124) within the canonical phosphate-binding loop (P loop: [I/V] HCXXGXXR[S/T]) (Figure 3B) (Lee et al., 1999). Together with its neighboring C2 domain, the phosphatase domain bares a number of surface exposed lysine and arginine residues which facilitate PTEN's association to the plasma membrane (Figure 3A) (Song et al., 2012). Other binding sites include a PIP<sub>2</sub> recognition region within PTEN's N-tail and a PDZ-binding motif at the C terminus (Campbell et al., 2003; Lee et al., 1999). So far, two strategies have been pursued to directly reduce PTEN's functional dose: (1) inhibition of PTEN's phosphatase activity and (2) inhibition of PTEN PPIs.

**Inhibition of Phosphatase Activity.** Similar to other protein tyrosine phosphatases (PTPs), PTEN has proven a challenging target with only a small number of inhibitors so far developed (Fahs et al., 2016; Stanford and Bottini, 2017). Early PTEN inhibitors originated from a screen of bisperoxovanadium (bpV) complexes with promiscuous PTP inhibitory activities (Salmena, 2016). Of these, complexes such as bpV-OHpic (Figure 3C) exhibit selectivity for PTEN above PTP- $\beta$  and PTP-1B, resulting in activation of AKT-dependent signaling in cell-based assays (Schmid et al., 2004). Subsequently, bpV complexes were utilized in a number of *in vivo* studies to inhibit PTEN and induce mTOR-mediated axon regeneration (Christie et al., 2010; Walker and Xu, 2014; Wu et al., 2013). Mechanistically, these complexes act via oxidation of PTEN's catalytic cysteine C124 resulting in the formation of a disulfide bond with closely aligned cysteine C71 (Figure 3D) (Lee et al., 2015). This oxidation is reversible and results in the formation of orthovanadate, which is known to inhibit various other human

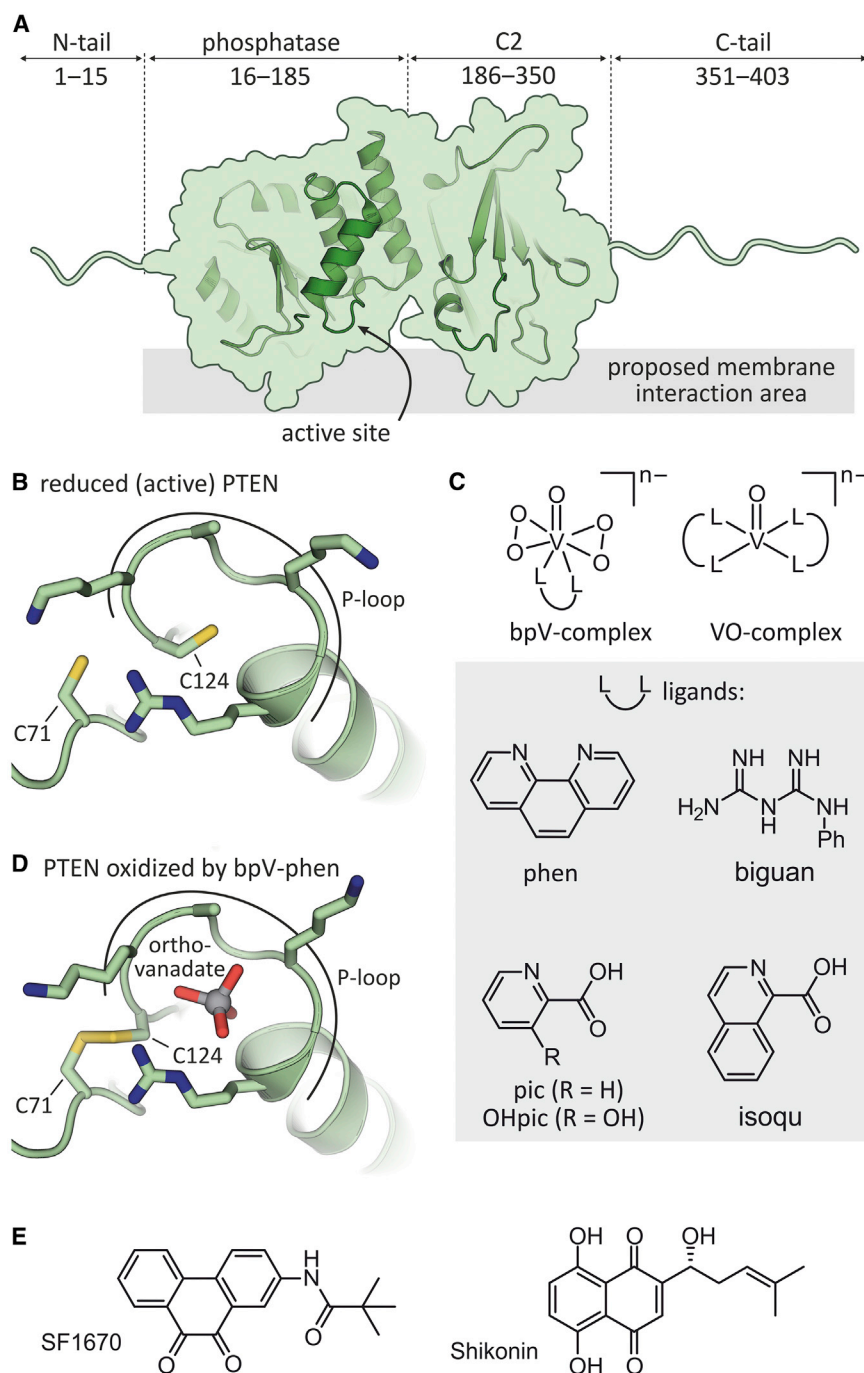
mechanisms of action (Garlich et al., 2005; Nigorikawa et al., 2006; Spinelli et al., 2015).

**Inhibition of Protein-Protein Interactions.** Inhibiting PPIs has also been explored to reduce PTEN functional dose. For this purpose, antagonistic molecules have been derived from PTEN itself. Esteban and co-workers synthesized a membrane-permeable variant of PTEN's PDZ-binding motif which they found to block post-synaptic PTEN membrane localization and reduce AKT/GSK3 $\beta$ -directed signaling in Alzheimer's mouse models (Knafo et al., 2016). Similarly, PDZ-derived peptide antagonists were capable of blocking MAST2-PTEN interactions (Terrien et al., 2012). In addition, other peptides derived from PTEN's phosphatase domain and C-tail have been found to positively influence axon growth and recovery in mice affected by spinal injury (Ohtake et al., 2014). Despite these results, the PTEN specificity of these molecules is intrinsically limited due to the ubiquity of PDZ motifs and recognition elements (Lee and Zheng, 2010). Alternatively, antagonists derived from PTEN interaction partners have been reported such as 3L4F, a truncated peptide from an intracellular loop of the 5-HT<sub>2C</sub> receptor (5-HT<sub>2C</sub>R), which was found to prevent PTEN-5-HT<sub>2C</sub>R complex formation and to decrease PTEN-mediated dephosphorylation both *in vitro* and *in vivo* (Anastasio et al., 2013; Ji et al., 2006).

### Targeting PTEN mRNA and PTEN Gene Editing

Inhibition of PTEN biogenesis has been mainly pursued using antisense oligonucleotides (ASOs). Comprised of DNA or non-natural analogs, ASOs target complementary mRNA strands through Watson-Crick base-pairing to prevent translational processing and/or induce nuclease-mediated degradation (Li and Rana, 2014). Initially reported ASOs targeting *PTEN* mRNA were comprised of phosphorothioate backbones and 2'-O-methoxy-ethyl (MOE)-modified ribonucleotides, which displayed strong biological profiles, reducing PTEN protein expression by up to 90% in mouse liver tissues (Butler et al., 2002). Further





**Figure 3. Inhibition of PTEN Phosphatase Activity**

(A) Schematic overview of PTEN's structure (derived from crystal structure PDB: 5BZZ) (Lee et al., 2015). (B) Close up of PTEN's active site not showing a tartrate molecule originating from crystallization buffer (PDB: 5BZZ) (Lee et al., 2015). (C) Selection of bpV and VO complexes exhibiting PTEN phosphatase inhibition. (D) Close up of PTEN's active site after bpV-mediated disulfide bridge formation (PDB: 5BUG) harboring orthovanadate (Lee et al., 2015). (E) Chemical structures of PTEN inhibitors.

case of *PTEN*-targeting shRNA, delivery via tyrosine-mutated adeno-associated virus (AAV) vectors induced mTOR-mediated axon regeneration in rat optic nerves (Huang et al., 2017).

Finally, rather than targeting *PTEN*'s gene products, proof-of-principle studies to directly inhibit *PTEN* transcription (antigene strategies) have been reported (Cox et al., 2015; Gutilla and Steward, 2016). By flanking *PTEN* with *LoxP* sequences, He and co-workers deleted *PTEN* in mouse sensorimotor cortices using an AAV-Cre-mediated system to induce mTOR-mediated corticospinal regeneration after injury (Liu et al., 2010). Notably, even after long-term (>12 months) *PTEN* deletion, cortical neurons displayed healthy phenotypes and did not display tumorigenesis (Gutilla et al., 2016).

#### Reduction of PTEN Dose:

#### Conclusions and Outlook

The design of selective and potent PTEN inhibitors remains an unresolved issue in drug discovery. Similar to other PTPs, this is mainly due to the highly polar nature of PTEN's active site, which hampers the development of cell-permeable inhibitors (Stanford and Bottini, 2017). For that reason, it is not surprising that reported PTEN inhibitors often follow a covalent and rather unselective mode of action involving the targeting of cysteine 124. Building on the susceptibility of this cysteine, covalent fragment-

based screening could be envisioned to identify more selective, irreversible inhibitors (Kathman et al., 2014; Ruddaraju and Zhang, 2017). Recent examples of allosteric and bivalent PTP inhibitors that target alternative sites may also open new options for the development of selective PTEN inhibitors (Zhang, 2017). Separately, the disruption of PTEN PPIs has shown potential in providing a means to selectively inhibit PTEN in defined disease contexts, potentially allowing for intervention with specific functions rather than the entire PIP<sub>3</sub>-dependent signaling network. While preliminary examples have mainly focused on

elaboration using locked nucleic acid (LNA) analogs yielded even greater potency but also led to hepatotoxicity *in vivo* (Swayze et al., 2007). Aside from ASOs, the therapeutic application of RNAi strategies (e.g., short interfering RNA [siRNA] and short hairpin RNA [shRNA]) has been explored with the support of specialized delivery modalities (Kanasty et al., 2013; Krishnamurthy et al., 2008). In one example, the use of lipopeptide nanoparticles allowed for the targeted delivery of *PTEN*-specific siRNAs to liver hepatocytes in mice, where PTEN expression levels were reduced by up to 80% (Dong et al., 2014). In the

antagonistic unmodified peptides, the use of peptidomimetic inhibitors should provide analogs with higher bioactivity (Pelay-Gimeno et al., 2015). In this respect, macrocyclic structures, derived from irregular loop-like binding epitopes are particularly interesting (Glas et al., 2014; Wiedmann et al., 2017). Addressing the low cellular uptake of peptide-derived structures, lessons learned from cell-penetrating peptides (Brock, 2014; Dietrich et al., 2017) or strategies that use smaller ligands that only form the product upon target engagement should be considered (Brauckhoff et al., 2014; Jaegle et al., 2017). To fully evaluate the potential of such strategies, a more detailed investigation of PTEN's interactome is required. In this context, the use of mixed modalities or the stabilization of certain PTEN PPIs could provide novel probes or potentially more selective agents (Thiel et al., 2012; Valeur et al., 2017). On a translational level, ASOs and RNAi strategies that target *PTEN* mRNA have proven useful for the modulation of PTEN's functional dose. However, well-documented delivery issues associated with these techniques are the main limiting factor for broader applications (Dowdy, 2017). Finally, the rise of novel gene editing techniques such as CRISPR/Cas 9, C2c2, or Cpf1 could offer potentially very efficient access to PTEN depletion in a tissue-specific manner provided that current delivery and selectivity issues have been addressed (Nakade et al., 2017).

### Increase of PTEN's Functional Dose

PTEN is a quasi-insufficient tumor suppressor referring to the fact that partial PTEN inactivation can already promote tumorigenesis (Carracedo et al., 2011). PTEN inactivation is seen in a variety of cancers with COSMIC listing over 3,000 *PTEN* mutations in 30 different tissue types. The bulk of these somatic mutations either disable PTEN's active site or alter its C2 domain to prevent membrane binding (Forbes et al., 2015). Therefore, increasing or re-instating PTEN's functional dose has been proposed as an anti-cancer strategy. Increasing its functional dose may also find application in other diseases related to PTEN inactivation, such as certain forms of autism or autism spectrum disorders where germline mutations in *PTEN* lead to increased synapse growth, manifesting in synaptic hyperactivity and excitability (Takeuchi et al., 2013; Knafo and Esteban, 2017). PTEN germline mutations can also lead to cancer predisposition syndromes such as Cowden disease, Bannayan-Riley-Ruvalcaba syndrome and Proteus syndrome (Arch et al., 1997; Hollander et al., 2011; Liaw et al., 1997). For that reason, increasing its functional dose is expected to benefit such patients. An increase of PTEN's functional dose is a particularly challenging endeavor, and depending on the disease context, this may require different strategies. So far, PTEN protein delivery, miRNA targeting, and gene editing have been pursued (Figure 2).

#### PTEN Protein Delivery

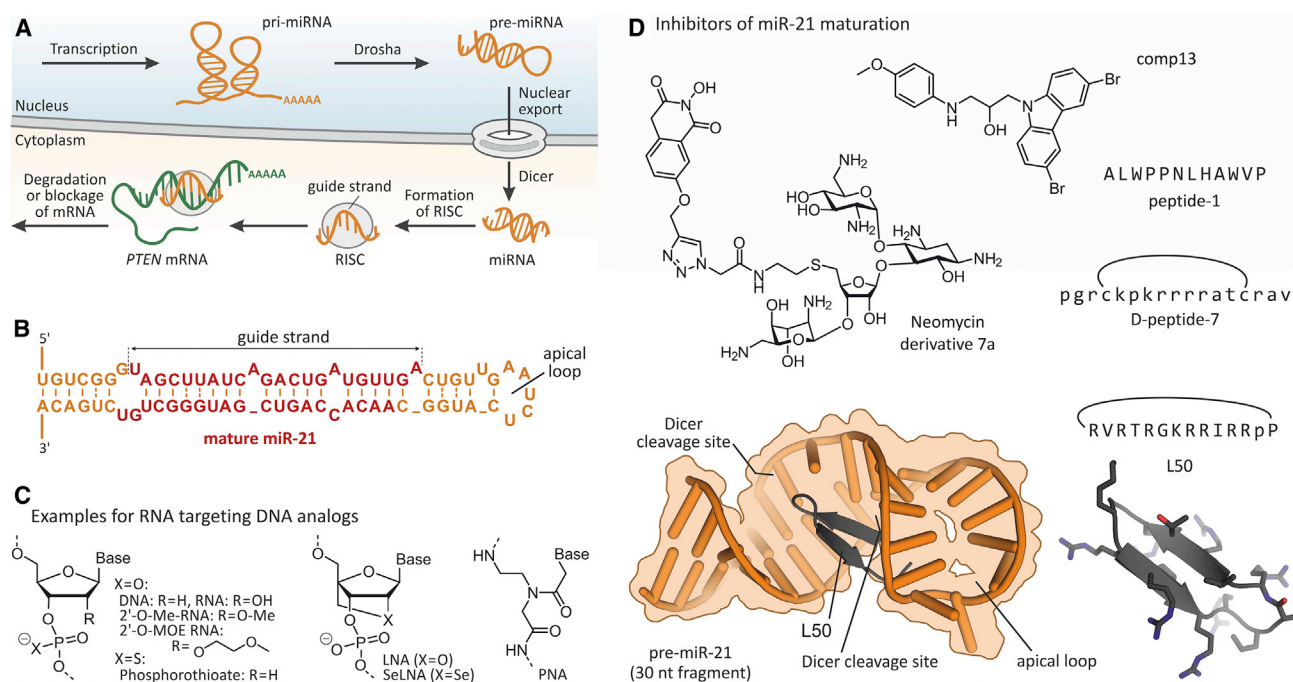
Besides antibodies, peptides, and hormones, a growing list of protein-based therapeutics have received regulatory approval in recent years (Kinch, 2015). While many issues have been overcome, therapeutic protein delivery remains challenging due to degradation and low membrane permeability (Mitragotri et al., 2014). Nonetheless, some studies indicate that the intracellular delivery of certain PTEN variants may be feasible. In one such approach, exogenous introduction of PTEN, functionalized with cationic lipidoid nanoparticles, promoted apoptosis of PTEN-

null, prostate cancer cells (PC-3) via the antagonism of AKT signaling (Altinoglu et al., 2016). Fluorescence microscopy of labeled PTEN nanoparticles confirmed intracellular delivery (Altinoglu et al., 2016). Similarly, it was found that silica nanoparticles also promote PTEN's cellular uptake (Arora and Ghosh, 2016). Alternatively, it was reported that a cell-permeable, translational variant of PTEN (PTEN-long) can inhibit PI3K signaling and induce tumor cell apoptosis *in vitro* as well as regression of PTEN-null xenograft tumors in mice (Hopkins et al., 2013).

#### Inhibition of PTEN-Targeting miRNAs

As *PTEN* mRNA is subject to translational repression by a host of miRNAs, miRNA inhibition provides a route to increase PTEN's functional dose. miRNAs are short, non-coding RNAs that are transcribed as part of large stem-loop-containing pri-miRNAs (Figure 4A). Pri-miRNAs are recognized by the RNase Drosha to provide smaller, hairpin-like sequences known as pre-miRNAs (Figure 4A). Upon nuclear export, pre-miRNAs undergo cleavage via the RNase Dicer to generate mature miRNA duplexes of ca. 21 bases in length with short unpaired terminal sequences (Figure 4A). One of the two strands of mature miRNA (guide strand) is then incorporated into the RNA-induced silencing complex (RISC) to recognize complementary or closely related mRNA sequences to block translation and/or promote mRNA degradation (Figure 4A) (Bartel, 2009; Lin and Gregory, 2015). RISC-associated miRNAs often recognize multiple mRNA targets due to their short length. Resultantly, many *PTEN*-targeting miRNAs also regulate other genes: e.g., miR-19 (*BIM*, *BCL2*, *Prkaa2*), miR-21 (*PDC4*, *RECK*, *TPM1*), and miR-221 (*BMF*, *BBC3/PUMA*, *CDKN1B*) (Krichevsky and Gabriely, 2009; Lupini et al., 2013; Mavrakis et al., 2010). In cancer, aberrantly transcribed miRNAs that dysregulate the mRNA of tumor suppressors and oncogenes have been termed oncomiRs (Esquela-Kerscher and Slack, 2006). One such oncomiR is the PTEN-targeting, miR-21, implicated in the progression of hepatocellular cancer, lung cancer, and colorectal cancer (Meng et al., 2007; Xiong et al., 2014; Zhang et al., 2010). miR-21 is a prime target for therapeutic application and its inhibition has been pursued intensively. For that reason, we focus here on miR-21 targeting as a means of increasing PTEN's functional dose.

**Direct Inhibition of Mature miR-21.** To target mature miR-21 guide strands (red in Figure 4B), a number of antisense oligonucleotides have been developed and are referred to as anti-miR-21s (Li and Rana, 2014). Following initial reports of 2'-OME anti-miR-21s (Figure 4C), Isis Pharmaceuticals performed a comprehensive screen of anti-miR-21 backbone modifications (Cheng et al., 2005; Davis et al., 2006). While both 2'-O-Me and 2'-O-MOE-modified derivatives (Figure 4C) showed comparable miR-21 affinity in biochemical assays, 2'-O-MOE anti-miR exhibited superior, cell-based miR-21 inhibition likely due to its higher nuclease stability (Davis et al., 2006). In separate studies, short phosphorothioate-based LNAs (Figure 4C) were used to engage the seed region of miR-21 with sub-nanomolar affinity resulting in long-lasting miR-21 inhibition *in vivo* (Obad et al., 2011). As a variation on this concept, anti-miR-21s have recently been assembled using selenomethylene-locked nucleic acids (SeLNA, Figure 4C) to further improve nuclease stability (Nahar et al., 2016a, 2016b). While the above-mentioned ASOs block miR-21, alternative approaches have aimed to degrade miR-21 (Lennox and Behlke, 2011). For this purpose, hybrid anti-miRs



**Figure 4. Inhibition of PTEN-targeting miRNAs**

(A) miRNA biogenesis and function involving pri- and pre-miRNA precursors that are processed by Drosha and Dicer, respectively.

(B) Sequence of precursor stem loop with mature miR-21 (red) and guide strand highlighted.

(C) Examples of oligonucleotide analogs used to construct miR-21-targeting ASOs.

(D) Chemical structures of miR-21 targeting molecules including NMR structure of L50 bound to truncated pre-miR-21 (30 nt, PDB: 5UZZ) (Shortridge et al., 2017).

containing both unmodified DNA and chemically modified building blocks have been employed to allow for RNase H degradation of miR-21 (Davis et al., 2006; Lennox and Behlke, 2010). In addition, catalytically active oligonucleotides have been developed that are capable of cleaving complementary single-stranded RNA. For example, hammerhead ribozymes were engineered to deplete miR-21 levels in human glioblastoma cells, resulting in increase of PTEN protein levels (Belter et al., 2016; Patutina et al., 2017).

**Inhibition of miR-21 Maturation.** Rather than directly engaging miRNAs, the inhibition of miRNA maturation has also been pursued (Schmidt, 2014; Shortridge and Varani, 2015). miRNA precursors are challenging therapeutic targets, owing to their flexibility, charged character, and lack of atypical ligand recognition motifs (Schmidt, 2014). While in principle, anti-miRs (such as those discussed above) can engage the sequences of miRNA precursors (e.g., pre-miR-21), they usually exhibit substantially lower affinities due to the self-complementarity of precursor hairpin structures. Alternatively, two classes of small molecules have been identified that display general RNA-binding tendencies. These include saccharide-derived structures that often target RNA loops as well as bulges, and aromatic scaffolds that intercalate within RNA duplexes (Thomas and Hergenrother, 2008; Velagapudi and Disney, 2013). For pre-miR-21 (Figure 4B), binding by bioactive aminoglycosides such as streptomycin, neomycin, and kanamycin has been reported, showing relatively low inhibition of Dicer cleavage (Bose et al., 2012; Yan et al., 2017). To increase potency, bifunctional derivatives combining pre-miR-21 binder neomycin with a small-molecule inhibitor of

Dicer have been developed. By virtue of conjugation, the neomycin derivative 7a (Figure 4D) saw an increase in Dicer inhibition by more than two orders of magnitude and was capable of selectively reducing miR-21 levels in cell-based assays (Yan et al., 2017). Alternatively, small-molecule screening campaigns for pre-miR-21 binders or maturation inhibitors have proven feasible, yielding a few relatively low affinity tool compounds (Connelly et al., 2017; Gumireddy et al., 2008; Naro et al., 2015; Shi et al., 2013). In one recent example, a microarray screen of 20,000 compounds provided comp13 (Figure 4D), which displays low micromolar affinity for pre-miR-21 and was found to inhibit Dicer cleavage in biochemical assays (Connelly et al., 2017).

To inhibit challenging biological targets such as pre-miRNA, peptides have recently attracted attention due to their large binding surfaces and unique conformational propensities (Pai et al., 2012). Using phage display, a linear, 12-mer peptide (peptide-1, Figure 4D) with high affinity for pre-miR-21 ( $K_d = 13$  nM) was found to inhibit Dicer processing in cell-based assays while also upregulating PTEN expression (Bose et al., 2015). In a separate study, mirror-image phage display of disulfide bridged peptides against pre-miR-21 was performed to address the inherent protease susceptibility of peptides. In this setup, L-peptides are screened against “mirror” RNA (L-enantiomer of RNA) with corresponding hit sequences then used as templates for D-peptides to bind natural D-RNA. In the case of pre-miR-21, this approach generated D-peptide-7 (Figure 4D), which displayed moderate affinity for pre-miR-21 in biochemical assays (Sakamoto et al., 2017). Recently, pre-miR-21 was also screened against a small



cyclic peptide library based on the RNA-binding domain of the bovine immunodeficiency virus Tat sequence. Using electromobility shift assays, cyclic peptide L50 (Figure 4D) was identified and later characterized as a selective, high-affinity pre-miR-21 binder ( $K_d = 0.2 \mu\text{M}$ ). In addition to inhibiting Dicer cleavage *in vitro*, a nuclear magnetic resonance (NMR) structure of pre-miR-21 in complex with peptide L50 was elucidated (Figure 4D). Interestingly, L50 binds to the major groove of the stem region adjacent to the apical loop thereby blocking sites of Dicer cleavage (Shortridge et al., 2017).

#### **PTEN Gene Introduction**

One final strategy that has briefly been described toward increasing PTEN's functional dose is *PTEN* gene introduction. First reported by Tanaka et al. in 2000, *PTEN* was exogenously introduced via an adenoviral vector into PTEN-null human bladder cancer cells where it was found to suppress tumor cell growth through the abrogation of AKT signaling (Tanaka et al., 2000). Subsequent studies involving human colorectal and prostate cancer cells yielded similar results (Saito et al., 2003; Tanaka et al., 2005). Moreover, for human bladder and colorectal cancer, gene editing successfully reduced tumor growth in xenograft mice (Saito et al., 2003; Tomioka et al., 2008). Notably, the introduction of additional *PTEN* genes into cells with physiological *PTEN* levels had only little effect, supporting the therapeutic applicability of this approach (Tanaka and Grossman, 2003). Even more remarkably, mice with systemically elevated *PTEN* ("Super-PTEN" mutants) display healthy phenotypes and are characterized with heightened resistance to cancer (Garcia-Cao et al., 2012).

#### **Increase of PTEN Dose: Conclusions and Outlook**

Overall, increasing *PTEN* functional dose represents an alternative to inhibitors of PI3K (responsible for PIP3 production at the membrane), AKT, or mTOR, most of which have faced efficacy issues related to therapeutic resistance (Porta et al., 2014). One way to achieve *PTEN* dose increase could involve the development of *PTEN* agonists or molecules that activate pathogenic *PTEN* variants. As shown for the discovery of allosteric SHIP-1 phosphatase activators, the screening of natural product libraries against *PTEN* could provide a novel source of such compounds (Ong et al., 2007). Another plausible *PTEN* activation strategy involves the design of bifunctional compounds to localize *PTEN* at the plasma membrane (Stiller et al., 2017) thereby promoting its phosphatase activity. As the case for protein delivery has been made above, engineered variants of *PTEN* with enhanced phosphatase activity, such as the recently reported ePTEN (Nguyen et al., 2014), may support a therapeutic application.

In regard to direct miR-21 targeting, the full breadth of available DNA analogs (e.g., PNA and morpholinos) has yet to be explored and can yield novel ASO-based inhibitors (van Rooij and Kauppinen, 2014). To circumvent the delivery issues associated with ASOs, however, the targeting of miRNA maturation is becoming increasingly investigated. With respect to small molecules, the utilization of dynamic combinatorial libraries or covalent inhibitor strategies can be expected to facilitate the discovery of novel pre-miR-21 ligands in the future (Connelly et al., 2016). Moreover, given recent achievements in phage display (Pai et al., 2012) and protein design (Chen et al., 2016) it is clear that peptide-derived structures also hold the potential to provide

selective pre- or pre-miR-21 binders. From initial screens, peptidomimetics such as peptoid ligands have exhibited suitability for this purpose (Chirayil et al., 2009; Diaz et al., 2014). The screening of alternative modalities such as aptamers appears to show similar promise and may be an alternative source of novel ligands (Kabza and Szczepanski, 2017). Having focused on miR-21, additional *PTEN*-targeting oncomiRs should also be considered and used to probe the suitability of miR-21 in the context of its other targets. Finally, with respect to gene therapy, many hurdles need to be overcome with regard to undesired immunogenicity and non-specific genetic modification (Kotterman et al., 2015). Once more, recent advances in CRISPR/Cas 9 gene editing and other systems provide a potentially powerful platform to correct for somatic *PTEN* mutations. However, considerable efforts are still required before such techniques see widespread therapeutic applications (Dai et al., 2016; Nakade et al., 2017; Xue et al., 2014).

#### **Concluding Remarks**

It is now 20 years since *PTEN*'s discovery. Within the first decade, many fundamental insights into *PTEN*'s phosphatase activity, its structure, and tumor suppressor function were pieced together. Passing into the second decade, large strides were made in understanding the extent and subtleties of *PTEN* regulation from the transcriptional level to PTMs. Having all these insights available, still many more questions regarding *PTEN* biology remain to be answered, e.g., What are the precise, nuclear roles of *PTEN*? How do phosphatase independent functions contribute to its tumor suppressor activity? What is the biological significance of *PTEN*'s growing list of isoforms and translational variants? To what degree does epigenetic regulation affect *PTEN* functional dose? How is *PTEN* dose affected by oncomiR networks?

The third decade can be expected to elucidate these remaining aspects of *PTEN* biology but also to contribute therapeutically relevant targeting strategies. In this respect, it is essential to identify disease contexts in which *PTEN* targeting is systemically tolerated. Particularly in regard to reducing its functional dose, *PTEN*'s "risky" profile as a tumor suppressor has to be considered. While recent studies suggest a possible therapeutic window for *PTEN* dose reduction without triggering tumorigenesis, dysfunctional outcomes of *PTEN* deletion in the past have raised questions over its therapeutic suitability (Gutilla et al., 2016; Liu et al., 2010; Pun et al., 2012; Williams et al., 2015). To address these issues, potent and selective inhibitors are required that allow selective, short-term *PTEN* inhibition preferably in a tissue-specific manner. In our view, such compounds will likely arise from protein- or mRNA-targeting approaches. In particular, when considering the availability of new targeting paradigms such as selective ribosomal inhibitors, spliceosome inhibitors, or targeted protein degradation approaches (e.g., PROTACS) (Cromm and Crews, 2017; León et al., 2017; Lintner et al., 2017). Undoubtedly, increasing *PTEN*'s functional dose is of prime interest as an anti-cancer strategy but is also extremely challenging, mainly due to a lack of *PTEN*-activating agents and general shortcomings related to miRNA targeting. It can be expected that all levels of *PTEN* biogenesis and regulation must be taken into consideration when aiming for therapeutically relevant *PTEN* dose reduction. In addition, it remains to be seen if



certain oncogenic PTEN variants are tractable as drug targets themselves, and if PTEN's post-translationally modified derivatives can be selectively modulated.

Taken together, we can conclude that PTEN is certainly an intriguing therapeutic target but that more efforts are required to define relevant indications both for an increase and a reduction of PTEN's functional dose. To address this question, chemical tools are required that allow selective modulation of the various PTEN functions. This process should be curiosity driven and consider all options, not only the protein's phosphatase activity, PPIs, and PTMs but also the *PTEN* gene and mRNA, including regulating miRNAs. For that reason, it is desirable that the different subfields move closer together and that resulting tool compounds are more rigorously tested in biologically relevant systems. With that in mind, one can certainly expect the chemical biology community to provide selective agents that may finally open up new pathways toward PTEN's pharmacological intervention.

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